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(FILE 'HOME' ENTERED AT 16:10:50 ON 26 DEC 2002)

FILE 'CAPLUS' ENTERED AT 16:22:23 ON 26 DEC 2002

L1 94394 S NAD##
L2 4559 S NAD(W)P
L3 4 S L2 AND CONFIGURATION AND (BIND? OR BOUND) AND (PEPTIDE OR POL
L4 95 S L2 (3A) (PEPTIDE OR POLYPEPTIDE OR PROTEIN)
L5 40 S L4 AND (CONFORM? OR STRUCTURE OR BIND?)
L6 35 S L5 NOT MECHANISM
L7 34 S L6 NOT (KINASE C)
L8 30 S L7 NOT RNA

=> d bib,kwic 1-30

L8 ANSWER 1 OF 30 CAPLUS COPYRIGHT 2002 ACS
AN 2002:799342 CAPLUS
TI Optical tomography of human skin with subcellular spatial and picosecond time resolution using intense near infrared femtosecond laser pulses
AU Koenig, Karsten; Wollina, Uwe; Riemann, Iris; Peukert, Christiane; Halbhuber, Karl-Juergen; Konrad, Helga; Fischer, Peter; Fuenfstueck, Veronika; Fischer, Tobias W.; Elsner, Peter
CS Laser Microscopy Div., Inst. Anatomy II, Univ. Jena, Jena, D-07740, Germany
SO Proceedings of SPIE-The International Society for Optical Engineering (2002), 4620(Multiphoton Microscopy in the Biomedical Sciences II), 191-201
CODEN: PSISDG; ISSN: 0277-786X
PB SPIE-The International Society for Optical Engineering
DT Journal
LA English
RE.CNT 16 THERE ARE 16 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT
AB We describe the novel high resoln. imaging tool DermaInspect 100 for non-invasive diagnosis of dermatol. disorders based on multiphoton autofluorescence imaging (MAI)and second harmonic generation. Femtosecond laser pulses in the spectral range of 750 nm to 850 nm have been used to image in vitro and in vivo human skin with subcellular spatial and picosecond temporal resoln. The non-linear induced autofluorescence originates mainly from naturally endogenous fluorophores/**protein structures** like **NAD**(**P**)H, flavins, keratin, collagen, elastin, porphyrins and melanin. Second harmonic generation was obsd. in the stratum corneum and in the dermis. The system with a wavelength-tunable compact 80 MHz Ti:sapphire laser, a scan module with galvo scan mirrors, piezoelec. objective positioner, fast photon detector and time-resolved single photon counting unit was used to perform optical sectioning and 3D autofluorescence lifetime imaging (t-mapping). In addn., a modified femtosecond laser scanning microscope was involved in autofluorescence measurements. Tissues of patients with psoriasis, nevi, dermatitis, basalioma and melanoma have been investigated. Individual cells and skin **structures** could be clearly visualized. Intracellular components and connective tissue **structures** could be further characterized by tuning the excitation wavelength in the range of 750 nm to 850 nm and by calcn. of mean fluorescence lifetimes per pixel and of particular regions of interest. The novel non-invasive imaging system provides 4D (x,y,z,t) optical biopsies with subcellular resoln. and offers the possibility to introduce a further optical diagnostic method in dermatol.

L8 ANSWER 2 OF 30 CAPLUS COPYRIGHT 2002 ACS
AN 2002:603004 CAPLUS
DN 137:306454
TI Molecular cloning and characterization of the gene coding for the aerobic

azoreductase from Xenophilus azovorans KF46F
AU Blumel, Silke; Knackmuss, Hans-Joachim; Stolz, Andreas
CS Institut fur Mikrobiologie der Universitat Stuttgart, Stuttgart, 70569, Germany
SO Applied and Environmental Microbiology (2002), 68(8), 3948-3955
CODEN: AEMIDF; ISSN: 0099-2240
PB American Society for Microbiology
DT Journal
LA English
RE.CNT 50 THERE ARE 50 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT
AB The gene coding for an aerobic azoreductase was cloned from Xenophilus azovorans KF46F (formerly Pseudomonas sp. strain KF46F), which was previously shown to grow with the carboxylated azo compd. 1-(4'-carboxyphenylazo)-2-naphthol (carboxy-Orange II) as the sole source of carbon and energy. The deduced amino acid sequence encoded a protein with a mol. wt. of 30,278 and showed no significant homol. to amino acid sequences currently deposited at the relevant data bases. A presumed NAD(P)H-**binding** site was identified in the amino-terminal region of the azoreductase. The enzyme was heterologously expressed in Escherichia coli and the azoreductase activities of resting cells and cell exts. were compared. The results suggested that whole cells of the recombinant E. coli strains were unable to take up sulfonated azo dyes and therefore did not show in vivo azoreductase activity. The turnover of several industrially relevant azo dyes by cell exts. from the recombinant E. coli strain was demonstrated.
IT **Protein** motifs
(**NAD(P)H-binding** site; mol. cloning and characterization of the gene coding for the aerobic azoreductase from Xenophilus azovorans KF46F)

L8 ANSWER 3 OF 30 CAPLUS COPYRIGHT 2002 ACS
AN 2002:145298 CAPLUS
TI Comparison of Human Chromosome 6p25 with Mouse Chromosome 13 Reveals a Greatly Expanded Ov-Serpin Gene Repertoire in the Mouse
AU Kaiserman, Dion; Knaggs, Susan; Scarff, Katrina L.; Gillard, Anneliese; Mirza, Ghazala; Cadman, Matthew; McKeone, Richard; Denny, Paul; Cooley, Jessica; Benarafa, Charaf; Remold-O'Donnell, Eileen; Ragoussis, Jiannis; Bird, Phillip I.
CS Department of Biochemistry and Molecular Biology, Monash University, 3800, Australia
SO Genomics (2002), 79(3), 349-362
CODEN: GNMCEP; ISSN: 0888-7543
PB Academic Press
DT Journal
LA English
RE.CNT 36 THERE ARE 36 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT
AB Ov-serpins are intracellular proteinase inhibitors implicated in the regulation of tumor progression, inflammation, and cell death. The 13 human ov-serpin genes are clustered at 6p25 (3 genes) and 18q21 (10 genes), and share common **structures**. We show here that a 1-Mb region on mouse chromosome 13 contains at least 15 ov-serpin genes compared with the three ov-serpin genes within 0.35 Mb at human 6p25 (SERPINB1 (MNEI), SERPINB6 (PI-6), SER-PINB9 (PI-9)). The mouse serpins have characteristics of functional inhibitors and fall into three groups on the basis of similarity to MNEI, PI-6, or PI-9. The genes map between the mouse orthologs of the Werner helicase interacting **protein** and **NAD(P)H** menadioine oxidoreductase 2 genes, in a region that contains the markers D13Mit136 and D13Mit116. They have the seven-exon **structure** typical of human 6p25 ov-serpin genes, with identical intron phasing. Most show restricted patterns of expression, with common sites of synthesis being the placenta and immune tissue. Compared with human, this larger mouse serpin repertoire probably reflects

the need to regulate a larger proteinase repertoire arising from differing evolutionary pressures on the reproductive and immune systems. (c) 2002 Academic Press.

L8 ANSWER 4 OF 30 CAPLUS COPYRIGHT 2002 ACS
AN 2001:267358 CAPLUS
DN 135:15850
TI NAD(P)H:menadione oxidoreductase of the amitochondriate eukaryote Giardia lamblia: a simpler homologue of the vertebrate enzyme
AU Sanchez, Lidya B.; Elmendorf, Heidi; Nash, Theodore E.; Muller, Miklos
CS Laboratory of Biochemical Parasitology, The Rockefeller University, New York, NY, 10021, USA
SO Microbiology (Reading, United Kingdom) (2001), 147(3), 561-570
CODEN: MROBEO; ISSN: 1350-0872
PB Society for General Microbiology
DT Journal
LA English
RE.CNT 31 THERE ARE 31 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT
AB The amitochondriate eukaryote Giardia lamblia contains an NAD(P)H:menadione oxidoreductase (EC 1.6.99.2) (glQR) that catalyzes the two-electron transfer oxidn. of NAD(P)H with a quinone as acceptor. The gene encoding this protein in G. lamblia was expressed in Escherichia coli. The purified recombinant **protein** had an **NAD(P)H** oxidoreductase activity, with NADPH being a more efficient electron donor than NADH. Menadione, naphthoquinone and several artificial electron acceptors served as substrate for the enzyme. The glQR protein shows high amino acid similarity to its homologs in vertebrates and also to a series of hypothetical proteins from bacteria. Although glQR is considerably smaller than the mammalian enzymes, three-dimensional modeling shows similar arrangement of the secondary structural elements. Most amino acid residues of the mammalian enzymes that participate in substrate **binding** or catalysis are conserved. Conservation of these features and the similarity in substrate specificity and in susceptibility to inhibitors establish glQR as an authentic member of this protein family.
IT Enzyme functional sites
(active; active site **structure** of menadione:oxidoreductase of Giardia lamblia)
IT Mammal (Mammalia)
(conservation of secondary **structure** of NAD(P)H menadione:oxidoreductases of Giardia lamblia and mammals)
IT Evolution
(mol., conservative; conservation of secondary **structure** of NAD(P)H menadione:oxidoreductases of Giardia lamblia and mammals)
IT Secondary **structure**
(protein; conservation of secondary **structure** of NAD(P)H menadione:oxidoreductases of Giardia lamblia and mammals)

L8 ANSWER 5 OF 30 CAPLUS COPYRIGHT 2002 ACS
AN 2000:615952 CAPLUS
DN 134:15548
TI Molecular characterization and localization of the NAD(P)H oxidase components gp91-phox and p22-phox in endothelial cells
AU Bayraktutan, Ulvi; Blayney, Lynda; Shah, Ajay M.
CS Departments of Cardiology, King's College, London, SE5 9PJ, UK
SO Arteriosclerosis, Thrombosis, and Vascular Biology (2000), 20(8), 1903-1911
CODEN: ATVBFA; ISSN: 1079-5642
PB Lippincott Williams & Wilkins
DT Journal
LA English
RE.CNT 55 THERE ARE 55 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

AB The prodn. of reactive oxygen species (ROS) within endothelial cells may have several effects, including alterations in the activity of paracrine factors, gene expression, apoptosis, and cellular injury. Recent studies indicate that a phagocyte-type NAD(P)H oxidase is a major source of endothelial ROS. In contrast to the high-output phagocytic oxidase, the endothelial enzyme has much lower biochem. activity and a different substrate specificity (NADH>NADPH). In the present study, we (1) cloned and characterized the cDNA and predicted amino acid **structures** of the 2 major subunits of rat coronary microvascular endothelial cell NAD(P)H oxidase, gp91-phox and p22-phox; (2) undertook a detailed comparison with phagocytic NADPH oxidase sequences; and (3) studied the subcellular location of these subunits in endothelial cells. Although these studies revealed an overall high degree of homol. (>90%) between the endothelial and phagocytic oxidase subunits, the endothelial gp91-phox sequence has potentially important differences in a putative NADPH-**binding** domain and in putative glycosylation sites. In addn., the subcellular location of the endothelial gp91-phox and p22-phox subunits is significantly different from that reported for the neutrophil oxidase, in that they are predominantly intracellular and collocated in the vicinity of the endoplasmic reticulum. This first detailed characterization of gp91-phox and p22-phox **structure** and location in endothelial cells provides new data that may account, in part, for the differences in function between the phagocytic and endothelial NAD(P)H oxidases.

IT **Protein** sequences
cDNA sequences
(of endothelial **NAD(P)**H oxidases of rat; mol. characterization and subcellular localization of NAD(P)H oxidase components gp91-phox and p22-phox in vascular endothelial cells)

L8 ANSWER 6 OF 30 CAPLUS COPYRIGHT 2002 ACS
AN 2000:444725 CAPLUS
DN 133:306968
TI Analysis of functional domains on glutamate synthase
AU Nalbantoglu, Barbaros
CS Department of Biochemistry, Faculty of Sciences and Arts, Ataturk University, Erzurum, Turk.
SO Turkish Journal of Biology (2000), 24(2), 197-213
CODEN: TJBIEZ; ISSN: 1300-0152
PB Scientific and Technical Research Council of Turkey
DT Journal; General Review
LA English
RE.CNT 56 THERE ARE 56 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT
AB A review with 56 refs. Glutamate synthases (GOGAT) were analyzed to identify the functional **binding** domains of the substrate (glutamine) and cofactors (FMN, NAD(P)H, FAD, [3Fe-4S]1+,0 and [4Fe-4S]2+,1+ clusters and ferredoxin) on this enzyme. The published amino acid sequences of six different NAD(P)H-dependent GOGATs (NAD(P)H-GOGAT) and ten different ferredoxin-dependent GOGATs (Fd-GOGAT) were used for this anal. The amino acid sequences of these sixteen GOGATs were compared with the amino acid sequences of aminotransferases for glutamine, flavoproteins for FMN, flavoproteins and pyridine-nucleotide-dependent enzymes for FAD and **NAD(P)**H, iron-sulfur **proteins** for [3Fe-4S]1+,0 and [4Fe-4S]2+,1+ clusters and ferredoxin-dependent enzymes for ferredoxin. It was detd. that Fd-GOGAT has one domain each for glutamine, FMN and [3Fe-4S]1+,0 cluster and two domains each for FAD and ferredoxin; the NADPH-GOGAT .alpha. subunit has the same domains as Fd-GOGAT except for the ferredoxin domains, and .beta. subunit has one domain each for NADPH and FAD and two domains for two [4Fe-4S]2+,1+ clusters; NADH-GOGAT has the same domains as NADPH-GOGAT.

L8 ANSWER 7 OF 30 CAPLUS COPYRIGHT 2002 ACS
AN 2000:404875 CAPLUS
DN 133:147280

TI New functions for the ancient globin family: bacterial responses to nitric oxide and nitrosative stress
AU Poole, Robert K.; Hughes, Martin N.
CS Krebs Inst. Biomol. Res., Univ. Sheffield, Sheffield, S10 2TN, UK
SO Molecular Microbiology (2000), 36(4), 775-783
CODEN: MOMIEE; ISSN: 0950-382X
PB Blackwell Science Ltd.
DT Journal; General Review
LA English
RE.CNT 36 THERE ARE 36 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT
AB A review with 36 refs. Globin-like O2-**binding** proteins occur in bacteria, yeasts and other fungi, and protozoa. The simplest contain protoheme as sole prosthetic group, but show considerable variation in their similarity to the classical animal globins and plant globins. FlavoHbs comprise a heme domain homologous to classical globins and a ferredoxin-NADP+ reductase (FNR)-like domain that converts the globin into an **NAD**(**P**)H-oxidizing **protein** with diverse reductase activities. In Escherichia coli, the prototype flavoHb (Hmp) is clearly involved in responses to NO and nitrosative stress: (i) the structural gene hmp is upregulated by NO and nitrosating agents; (ii) purified Hmp **binds** NO avidly, but also converts it to NO3- (aerobically) or N2O (anaerobically); (iii) hmp mutants are hypersensitive to NO and nitrosative stresses. Here, recent advances in E. coli and the growing no. of microbes in which globins are known are reviewed, with particular attention to the essential chem. of NO and related reactive spp., and their interactions with globins, and it is suggested that microbial globins have addnl. functions unrelated to "NO" stresses.

L8 ANSWER 8 OF 30 CAPLUS COPYRIGHT 2002 ACS
AN 2000:270487 CAPLUS
DN 133:1100
TI 5-Hydroxytryptamine1A receptor/Gi.beta..gamma. stimulates mitogen-activated **protein** kinase via **NAD**(**P**)H oxidase and reactive oxygen species upstream of Src in Chinese hamster ovary fibroblasts
AU Mukhin, Yurii V.; Garnovskaya, Maria N.; Collinsworth, Georgiann; Grewal, Jasjit S.; Pendergrass, DeKisha; Nagai, Toshio; Pinckney, Stephen; Greene, Eddie L.; Raymond, John R.
CS Department of Medicine, Medical University of South Carolina, Charleston, SC, 29425, USA
SO Biochemical Journal (2000), 347(1), 61-67
CODEN: BIJOAK; ISSN: 0264-6021
PB Portland Press Ltd.
DT Journal
LA English
RE.CNT 52 THERE ARE 52 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT
TI 5-Hydroxytryptamine1A receptor/Gi.beta..gamma. stimulates mitogen-activated **protein** kinase via **NAD**(**P**)H oxidase and reactive oxygen species upstream of Src in Chinese hamster ovary fibroblasts
IT G proteins (guanine nucleotide-**binding** proteins)
RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)
(Gi (adenylate cyclase-inhibiting); 5-hydroxytryptamine1A receptor coupled to Gi.beta..gamma. stimulates MAP kinase via NAD(P)H oxidase and reactive oxygen species upstream of Src in Chinese hamster ovary fibroblasts)

L8 ANSWER 9 OF 30 CAPLUS COPYRIGHT 2002 ACS
AN 2000:26761 CAPLUS
DN 132:148287
TI New sequence motifs in flavoproteins: evidence for common ancestry and

tools to predict **structure**
AU Vallon, Olivier
CS Institute de Biologie Physico-Chimique, CNRS, Paris, F-75005, Fr.
SO Proteins: Structure, Function, and Genetics (2000), 38(1), 95-114
CODEN: PSFGEY; ISSN: 0887-3585
PB Wiley-Liss, Inc.
DT Journal
LA English
RE.CNT 104 THERE ARE 104 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT
TI New sequence motifs in flavoproteins: evidence for common ancestry and tools to predict **structure**
AB We describe two new sequence motifs, present in several families of flavoproteins. The "GG motif" (RxGGRxxS/T) is found shortly after the .beta..alpha..beta.dinucleotide-**binding** motif (DBM) in L-amino acid oxidases, achacin and aplysianin-A, monoamine oxidases, corticosteroid-**binding** proteins, and tryptophan 2-monooxygenases. Other disperse sequence similarities between these families suggest a common origin. AGG motif is also found in protoporphyrinogen oxidase and carotenoid desaturases and, reduced to the central GG doublet, in the TH14 protein, dTDP-4-dehydrorhamnose reductase, sol. fumarate reductase, steroid dehydrogenases, Rab GDP-dissocn. inhibitor, and in most flavoproteins with two dinucleotide-**binding** domains (glutathione reductase, glutamate synthase, flavin-contg. monooxygenase, trimethylamine dehydrogenase...). In the latter families, an "ATG motif" (oxhhhATG) is found in both the FAD- and NAD(P)H-**binding** domains, forming the fourth .beta.-strand of the Rossman fold and the connecting loop. On the basis of these and previously described motifs, we present a classification of dinucleotide-**binding** proteins that could also serve as an evolutionary scheme. Like the DBM, the ATG motif appears to predate the divergence of NAD(P)H- and FAD-**binding** proteins. We propose that flavoproteins have evolved from a well-differentiated **NAD(P)H-binding protein**. The bulk of the substrate-**binding** domain was formed by an insertion after the fourth .beta.-strand, either of a closely related NAD(P)H-**binding** domain or of a domain of completely different origin.
IT Proteins, specific or class
RL: PRP (Properties)
(FAD-**binding**; new sequence motifs in flavoproteins: evidence for common ancestry and tools to predict **structure**)
IT **Proteins**, specific or class
RL: PRP (Properties)
(**NAD(P)H-binding**; new sequence motifs in flavoproteins: evidence for common ancestry and tools to predict **structure**)
IT Proteins, specific or class
RL: PRP (Properties)
(Rossman-type; new sequence motifs in flavoproteins: evidence for common ancestry and tools to predict **structure**)
IT Proteins, specific or class
RL: PRP (Properties)
(dinucleotide-**binding**; new sequence motifs in flavoproteins: evidence for common ancestry and tools to predict **structure**)
IT Enzymes, properties
RL: PRP (Properties)
(flavin-contg.; new sequence motifs in flavoproteins: evidence for common ancestry and tools to predict **structure**)
IT Protein sequences
(homol.; new sequence motifs in flavoproteins: evidence for common ancestry and tools to predict **structure**)
IT Evolution
(mol.; new sequence motifs in flavoproteins: evidence for common ancestry and tools to predict **structure**)

IT Protein motifs
(new sequence motifs in flavoproteins: evidence for common ancestry and tools to predict **structure**)
IT Flavoproteins
RL: PRP (Properties)
(new sequence motifs in flavoproteins: evidence for common ancestry and tools to predict **structure**)
IT **Conformation**
(protein; new sequence motifs in flavoproteins: evidence for common ancestry and tools to predict **structure**)
IT Enzyme functional sites
(substrate-**binding**; new sequence motifs in flavoproteins: evidence for common ancestry and tools to predict **structure**)
IT 9035-82-9, Dehydrogenase 9038-14-6, Flavin-contg. monooxygenase
RL: PRP (Properties)
(new sequence motifs in flavoproteins: evidence for common ancestry and tools to predict **structure**)

L8 ANSWER 10 OF 30 CAPLUS COPYRIGHT 2002 ACS
AN 1999:286792 CAPLUS
DN 131:99211
TI Crystal **structure** of NAD(P)H:flavin oxidoreductase from Escherichia coli
AU Ingelman, Margareta; Ramaswamy, S.; Niviere, Vincent; Fontecave, Marc; Eklund, Hans
CS Department of Molecular Biology, Swedish University of Agricultural Sciences Biomedical Center, Uppsala, S-751 24, Swed.
SO Biochemistry (1999), 38(22), 7040-7049
CODEN: BICHAW; ISSN: 0006-2960
PB American Chemical Society
DT Journal
LA English
RE.CNT 49 THERE ARE 49 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT
TI Crystal **structure** of NAD(P)H:flavin oxidoreductase from Escherichia coli
AB Flavin reductases use flavins as substrates and are distinct from flavoenzymes which have tightly bound flavins. The reduced flavin can serve to reduce ferric complexes and Fe proteins. In E. coli, reactivation of ribonucleotide reductase is achieved by reduced flavins produced by flavin reductase. The crystal **structure** of E. coli NAD(P)H-flavin reductase detd. here revealed that the enzyme **structure** was similar to the **structures** of the ferredoxin reductase family of flavoproteins despite very low sequence similarities. The main difference between the flavin reductase and structurally related flavoproteins was that there was no **binding** site for the AMP moiety of FAD. The direction of the helix in the flavin **binding** domain, corresponding to the phosphate **binding** helix in the flavoproteins, was also slightly different and less suitable for phosphate **binding**. The interactions for flavin substrates were instead provided by a hydrophobic isoalloxazine **binding** site that also contained a Ser and a Thr residue, which formed H-bonds to the isoalloxazine of bound riboflavin in a substrate complex.
ST flavin reductase crystal **structure** Escherichia
IT Escherichia coli
(crystal **structure** of NAD(P)H-flavin reductase from Escherichia coli)
IT Crystal growth
Crystal **structure**
(of NAD(P)H-flavin reductase from Escherichia coli)
IT **Conformation**
(**protein**; of **NAD(P)**H-flavin reductase from Escherichia coli)
IT 64295-83-6, NAD(P)H-flavin reductase

RL: PEP (Physical, engineering or chemical process); PRP (Properties); PROC (Process)
(crystal **structure** of NAD(P)H-flavin reductase from Escherichia coli)

L8 ANSWER 11 OF 30 CAPLUS COPYRIGHT 2002 ACS
AN 1998:422047 CAPLUS
DN 129:158428
TI New insights for dinucleotide backbone **binding** in conserved C5'-H... O hydrogen bonds
AU Chu, Pei-Ying; Hwang, Ming-Jing
CS Division of Structural Biology, Inst. Biomed. Sci., Inst. Biomedical Sci., Taipei, Taiwan
SO Journal of Molecular Biology (1998), 279(4), 695-701
CODEN: JMOBAK; ISSN: 0022-2836
PB Academic Press Ltd.
DT Journal
LA English
RE.CNT 17 THERE ARE 17 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT
TI New insights for dinucleotide backbone **binding** in conserved C5'-H... O hydrogen bonds
AB Most enzymes that utilize dinucleotide NAD or NADP are known to comprise a glycine-rich loop segment (e.g. the GXGXXG signature motif of Rossman fold) which **binds** the cofactor's diphosphate moiety. Through anal. of a set of diverse **NAD(P)**-bound **protein structures**, we show here that with few exceptions this diphosphate **binding** is complemented by a second loop segment interacting from a different angle with unconventional yet apparently ubiquitous C-H...O hydrogen bonds formed between C5' methylene of dinucleotide and, primarily, carbonyl oxygen of protein. This finding implicates an important role of C5' in protein-nucleotide recognition.
IT Enzyme functional sites
(cofactor-**binding**; unconventional hydrogen bonding in nicotinamide dinucleotide cofactor recognition by enzymes)

L8 ANSWER 12 OF 30 CAPLUS COPYRIGHT 2002 ACS
AN 1997:584258 CAPLUS
DN 127:259159
TI Identifying the major proteome components of Haemophilus influenzae type-strain NCTC 8143
AU Link, Andrew J.; Hays, Lara G.; Carmack, Edwin B.; Yates, John R., III
CS Dep. Molecular Biotechnology, Washington Univ., Seattle, WA, 98195, USA
SO Electrophoresis (1997), 18(8), 1314-1334
CODEN: ELCTDN; ISSN: 0173-0835
PB Wiley-VCH
DT Journal
LA English
IT Proteins, specific or class
RL: BOC (Biological occurrence); BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study); OCCU (Occurrence)
(ATP-**binding**, Methylgalactoside permease ATP-**binding** protein; proteins of Haemophilus influenzae type-strain NCTC 8143, sequence anal., isoelec. point, and gene expression)
IT Proteins, specific or class
RL: BOC (Biological occurrence); BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study); OCCU (Occurrence)
(galactoside-**binding**, Periplasmic; proteins of Haemophilus influenzae type-strain NCTC 8143, sequence anal., isoelec. point, and gene expression)
IT Proteins, specific or class
RL: BOC (Biological occurrence); BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study); OCCU (Occurrence)
(glutamine-**binding**, periplasmic; proteins of Haemophilus

influenzae type-strain NCTC 8143, sequence anal., isoelec. point, and gene expression)

IT Proteins, specific or class
RL: BOC (Biological occurrence); BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study); OCCU (Occurrence)
(phosphate-**binding**, Periplasmic; proteins of Haemophilus influenzae type-strain NCTC 8143, sequence anal., isoelec. point, and gene expression)

IT Proteins, specific or class
RL: BOC (Biological occurrence); BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study); OCCU (Occurrence)
(precursor, Major ferric iron **binding** protein precursor; proteins of Haemophilus influenzae type-strain NCTC 8143, sequence anal., isoelec. point, and gene expression)

IT Proteins, specific or class
RL: BOC (Biological occurrence); BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study); OCCU (Occurrence)
(ribose-**binding**, Periplasmic; proteins of Haemophilus influenzae type-strain NCTC 8143, sequence anal., isoelec. point, and gene expression)

IT 9000-97-9, Aspartate aminotransferase 9001-18-7, Lipoamide dehydrogenase 9001-48-3, Glutathione reductase 9001-50-7, Glyceraldehyde-3-phosphate dehydrogenase 9001-52-9, Fructose-1,6-bisphosphatase 9001-60-9, Lactate dehydrogenase 9001-64-3, Malate dehydrogenase 9001-69-8, Ornithine carbamoyltransferase 9001-83-6, Phosphoglycerate kinase 9013-02-9, Adenylate kinase 9013-10-9, Glucosamine-6-phosphate deaminase 9014-08-8, Enolase 9014-12-4, Polynucleotide phosphorylase 9014-20-4, Pyruvate dehydrogenase 9015-76-3, Methionyl-tRNA formyltransferase 9015-83-2, Phosphoribosylpyrophosphate synthetase 9023-46-5, Threonyl-tRNA synthetase 9023-48-7, Seryl-tRNA synthetase 9023-56-7, CTP synthetase 9023-57-8, Adenylosuccinate synthetase 9023-58-9, Argininosuccinate synthetase 9023-78-3, Triosephosphate isomerase 9023-93-2, Acetyl-coenzyme A carboxylase 9024-00-4, Tryptophanase 9024-32-2, Dihydroxyacid dehydrase 9024-52-6, Fructose-bisphosphate aldolase 9024-82-2, Inorganic pyrophosphatase 9026-39-5, Uridine kinase 9026-69-1, Carbamate kinase 9027-30-9, Aspartase 9027-42-3, Acetate kinase 9027-60-5, N-Acetylneuraminate lyase 9027-73-0, 5'-Nucleotidase 9029-83-8, Serine hydroxymethyltransferase 9030-21-1, Purine-nucleoside phosphorylase 9030-22-2, Uridine phosphorylase 9030-24-4, Uracil phosphoribosyltransferase 9030-66-4, Glycerol kinase 9030-90-4, Phosphoserine aminotransferase 9031-02-1, 2-Oxoglutarate dehydrogenase 9032-29-5, Dihydrolipoamide acetyltransferase 9032-62-6, Phosphoglyceromutase 9032-89-7, Udp-glucose 4-epimerase 9037-18-7, 2',3'-Cyclic-nucleotide 2'-phosphodiesterase 9037-44-9, Exonuclease III 9037-67-6, .gamma.-Aminobutyric acid transaminase 9054-65-3, Branched-chain-amino-acid transaminase 9054-89-1, Superoxide dismutase 9055-59-8, Dihydrodipicolinate synthetase 9055-68-9, Prolyl-tRNA synthetase 9068-29-5, Tetrahydropteroyltriglutamate Methyltransferase 9068-76-2, Glutamyl-tRNA synthetase 9074-14-0, Thioredoxin reductase 9075-29-0, Phosphoglycerate dehydrogenase 9075-71-2, Biotin carboxylase 37205-35-9, Arginyl-tRNA synthetase 37250-34-3, 3-Ketoacyl-acyl carrier protein reductase 37290-89-4, Cysteine synthetase 37341-55-2, Phosphoenolpyruvate carboxykinase 54596-29-1, .gamma.-Glutamyl phosphate reductase 64295-83-6, **NAD(P)**H-flavin oxidoreductase 72162-89-1, TRNA-guanine transglycosylase 76106-82-6, Ribonuclease E 85030-75-7, ADP-L-glycero-D-mannoheptose-6-epimerase 142298-62-2, Short chain alcohol dehydrogenase
RL: BOC (Biological occurrence); BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study); OCCU (Occurrence)
(**proteins** of Haemophilus influenzae type-strain NCTC 8143, sequence anal., isoelec. point, and gene expression)

L8 ANSWER 13 OF 30 CAPLUS COPYRIGHT 2002 ACS
AN 1997:306640 CAPLUS

DN 127:14789
TI NADP-dependent enzymes: I: Conserved stereochemistry of cofactor **binding**
AU Carugo, Oliviero; Argos, Patrick
CS European Molecular Biology Laboratory, Heidelberg, 69012, Germany
SO Proteins: Structure, Function, and Genetics (1997), 28(1), 10-28
CODEN: PSFGEY; ISSN: 0887-3585
PB Wiley-Liss
DT Journal
LA English
TI NADP-dependent enzymes: I: Conserved stereochemistry of cofactor **binding**
AB The ubiquitous redox cofactors, nicotinamide adenine dinucleotides (NAD and NADP), are very similar mols., despite their participation in substantially different biochem. processes. NADP differs from NAD in only the presence of an addnl. phosphate group esterified to the 2'-hydroxyl group of the ribose at the adenine end and yet NADP is confined with few exceptions to the reactions of reductive biosynthesis, whereas NAD is used almost exclusively in oxidative degrdns. The discrimination between NAD and NADP is therefore an impressive example of the power of mol. recognition by proteins. The many known tertiary **structures** of NADP complexes affords the possibility for an anal. of their discrimination. A systematic anal. of several crystal **structures** of **NAD(P)-protein** complexes show that: (1) the NADP coenzymes are more flexible in **conformation** than those of NAD; (2) although the protein-cofactor interactions are largely conserved in the NAD complexes, they are quite variable in those of NADP; and (3) in both cases the pocket around the nicotinamide moiety is substrate dependent. The conserved and variable interactions between protein and cofactors in the resp. **binding** pockets are reported in detail. Discrimination between NAD and NADP is essentially a consequence of the overall pocket and not of a few residues. A clear fingerprint in NAD complexes is a carboxylate side chain that chelates the diol group at the ribose near the adenine, whereas in NADP complexes an arginine side chain faces the adenine plane and interacts with the phosphomonoester. The latter type of interaction might be a general feature of recognition of nucleotides by proteins. Other features such as strand-like hydrogen bonding between the NADP diphosphate moieties and the protein are also significant. The NADP **binding** pocket properties should prove useful in protein engineering and design.
ST enzyme NAD NADP **binding** stereochem
IT Enzymes, biological studies
RL: BPR (Biological process); BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study); PROC (Process)
(NAD and NADP-dependent; conserved stereochem. of cofactor **binding** in NAD(P)-dependent enzymes)
IT Enzyme functional sites
(cofactor-**binding**; conserved stereochem. of cofactor **binding** in NAD(P)-dependent enzymes)
IT **Conformation**
Molecular recognition
(conserved stereochem. of cofactor **binding** in NAD(P)-dependent enzymes)
IT 53-59-8, NADP 53-84-9, NAD
RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)
(conserved stereochem. of cofactor **binding** in NAD(P)-dependent enzymes)

L8 ANSWER 14 OF 30 CAPLUS COPYRIGHT 2002 ACS
AN 1997:200448 CAPLUS
DN 126:260851
TI Characterization of the NAD(P)H-plastoquinone-oxidoreductase from maize thylakoid membranes

AU Funk, Edgar; Steinmueller, Klaus
CS Institut fur Entwicklungs- und Molekularbiologie der Pflanzen, Heinrich-Heine-Universitat, Dusseldorf, 40225, Germany
SO Photosynthesis: From Light to Biosphere, Proceedings of the International Photosynthesis Congress, 10th, Montpellier, Fr., Aug. 20-25, 1995 (1995), Volume 2, 701-704. Editor(s): Mathis, Paul. Publisher: Kluwer, Dordrecht, Neth.
CODEN: 64DFAW
DT Conference
LA English
IT Quaternary **structure**
(**protein**; of **NAD**(**P**)H-plastoquinone reductase from maize thylakoid membranes)

L8 ANSWER 15 OF 30 CAPLUS COPYRIGHT 2002 ACS
AN 1997:1222 CAPLUS
DN 126:101731
TI The NADH-**binding** subunit of respiratory chain complex I is nuclear-encoded in plants and identified only in mitochondria
AU Grohmann, Lutz; Rasmusson, Allan G.; Heiser, Volker; Thieck, Oliver; Brennicke, Axel
CS Institut Genbiologische Forschung Berlin, Berlin, D-14195, Germany
SO Plant Journal (1996), 10(5), 793-803
CODEN: PLJUED; ISSN: 0960-7412
PB Blackwell
DT Journal
LA English
TI The NADH-**binding** subunit of respiratory chain complex I is nuclear-encoded in plants and identified only in mitochondria
AB In higher plants, genes for subunits of respiratory chain complex I (NADH:ubiquinone oxidoreductase) have so far been identified solely in organellar genomes. At least nine subunits are encoded by the mitochondrial DNA and 11 homologs by the plastid DNA. One of the 'key' components of complex I is the subunit **binding** the substrate NADH. The corresponding gene for the mitochondrial subunit has now been cloned and identified in the nuclear genome from potato (Solanum tuberosum). The mature protein consists of 457 amino acids and is preceded by a mitochondrial targeting sequence of 30 amino acids. The protein is evolutionarily related to the NADH-**binding** subunits of complex I from other eukaryotes and is well conserved in the structural domains predicted for **binding** the substrate NADH, the FMN and one iron-sulfur cluster. Expression examd. in different potato tissues by Northern blot anal. shows the highest steady-state mRNA levels in flowers. Precursor proteins translated in vitro from the cDNA are imported into isolated potato mitochondria in a .DELTA..psi.-dependent manner. The processed translation product has an apparent mol. mass of 55 kDa, identical to the mature protein present in the purified plant mitochondrial complex I. However, the in vitro translated protein is not imported into isolated chloroplasts. To further investigate whether the complex I-like enzyme in chloroplasts contains an analogous subunit for **binding** of **NAD**(**P**)H, different plastid **protein** fractions were tested with a polyclonal antiserum directed against the bovine 51 kDa NADH-**binding** subunit. In none of the different thylakoid or stroma protein fractions analyzed were specific cross-reactive polypeptides detected. These results are discussed particularly with respect to the **structure** of a potential complex I in chloroplasts and the nature of its acceptor site.
IT Electron transport system, biological
Mitochondria
Potato (Solanum tuberosum)
Protein sequences
cDNA sequences
(NADH-**binding** subunit of respiratory chain complex I is nuclear-encoded in plants and identified only in mitochondria)

IT Gene, plant
RL: PRP (Properties)
(NADH-**binding** subunit of respiratory chain complex I is nuclear-encoded in plants and identified only in mitochondria)
IT 9079-67-8, Dehydrogenase, reduced nicotinamide adenine dinucleotide
RL: PRP (Properties)
(NADH-**binding** subunit of respiratory chain complex I is nuclear-encoded in plants and identified only in mitochondria)
IT 185830-52-8
RL: PRP (Properties)
(amino acid sequence; NADH-**binding** subunit of respiratory chain complex I is nuclear-encoded in plants and identified only in mitochondria)
IT 162486-42-2, GenBank X83999
RL: PRP (Properties)
(nucleotide sequence; NADH-**binding** subunit of respiratory chain complex I is nuclear-encoded in plants and identified only in mitochondria)

L8 ANSWER 16 OF 30 CAPLUS COPYRIGHT 2002 ACS
AN 1996:573121 CAPLUS
DN 125:240912
TI The nicotinamide dinucleotide **binding** motif: a comparison of nucleotide **binding** proteins
AU Bellamacina, Cornelia R.
CS Rosenstiel Basic Medical Sciences Research Center, Brandeis University, Waltham, MA, 02254-9110, USA
SO FASEB Journal (1996), 10(11), 1257-1269
CODEN: FAJOEC; ISSN: 0892-6638
PB Federation of American Societies for Experimental Biology
DT Journal; General Review
LA English
TI The nicotinamide dinucleotide **binding** motif: a comparison of nucleotide **binding** proteins
AB A review with 47 refs. Classical NAD (NAD+) **binding** proteins contain a .beta..alpha..beta..alpha..beta. unit. By comparing 14 such proteins, it is obsd. that an addnl. .beta. strand assocs. with this unit to form the core topol., the min. **structure** necessary to **bind** cofactor. Although the overall topologies of the cofactor **binding** domains of nicotinamide **binding** proteins vary, they all contain at least the core topol. The first 30-35 amino acids of the core topol., called the fingerprint region, are diagnostic for the presence of a dinucleotide **binding** fold. There are four characteristics of this fingerprint region: (1) a phosphate **binding** consensus sequence , GXGXXG, (2) six positions usually occupied by small hydrophobic amino acids, (3) a conserved, neg. charged residue (Glu or Asp) at the end of the second .beta. strand of the fingerprint region, and (4) a conserved pos. charged residue (Arg or Lys) at the beginning of the first .beta. strand of the fingerprint region. The core topologies of the classical nicotinamide **binding** proteins overlap well with root mean squared deviations of main chain atoms ranging from 0.7 to 4.7 .ANG.. A conserved interaction (found in 8 of the 12 classical nicotinamide **binding** proteins studied) between the cofactor and the protein is a hydrogen bond between the pyrophosphate oxygen of NAD(P)+ and the carboxy-terminal glycine of the phosphate **binding** helix, the first .alpha. helix of the .beta..alpha..beta..alpha..beta. unit. The classical nicotinamide **binding** proteins all **bind** their cofactor in the same location and orientation, with the cofactor itself adopting a similar extended conformation in every structure. Although obsd. less frequently than the classical fold, numerous nonclassical folding patterns are also used by **proteins** that **bind** **NAD(P)+**.
ST review nicotinamide dinucleotide **binding** motif protein

IT Phosphate group
(**binding** site; nicotinamide dinucleotide **binding** motif of nucleotide **binding** proteins)
IT **Conformation** and **Conformers**
(nicotinamide dinucleotide **binding** motif of nucleotide **binding** proteins)
IT Molecular orientation
(of cofactor; nicotinamide dinucleotide **binding** motif of nucleotide **binding** proteins)
IT Proteins, specific or class
RL: BPR (Biological process); BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study); PROC (Process)
(NAD-**binding**, nicotinamide dinucleotide **binding** motif of nucleotide **binding** proteins)
IT Enzymes
RL: BPR (Biological process); BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study); PROC (Process)
(NAD-dependent, nicotinamide dinucleotide **binding** motif of nucleotide **binding** proteins)
IT Nucleotides, biological studies
RL: BPR (Biological process); BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study); PROC (Process)
(di-, nicotinamide adenine contg.; nicotinamide dinucleotide **binding** motif of nucleotide **binding** proteins)
IT Protein sequences
(homol., nicotinamide dinucleotide **binding** motif of nucleotide **binding** proteins)
IT 9001-48-3, Glutathione reductase 9001-60-9, Lactate dehydrogenase
RL: BSU (Biological study, unclassified); MSC (Miscellaneous); PRP (Properties); BIOL (Biological study)
(-like proteins; nicotinamide dinucleotide **binding** motif of nucleotide **binding** proteins)
IT 53-59-8, NADP 53-84-9, NAD
RL: BPR (Biological process); BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study); PROC (Process)
(nicotinamide dinucleotide **binding** motif of nucleotide **binding** proteins)

L8 ANSWER 17 OF 30 CAPLUS COPYRIGHT 2002 ACS
AN 1995:991855 CAPLUS
DN 124:78167
TI A tactile sensory system of Myxococcus xanthus involves an extracellular **NAD(P)**+-containing **protein**
AU Lee, Bheong-Uk; Lee, Keesoo; Mendez, Jacqueline; Shimkets, Lawrence J.
CS Dep. Microbiol., Univ. Georgia, Athens, GA, 30602, USA
SO Genes & Development (1995), 9(23), 2964-73
CODEN: GEDEEP; ISSN: 0890-9369
PB Cold Spring Harbor Laboratory Press
DT Journal
LA English
TI A tactile sensory system of Myxococcus xanthus involves an extracellular **NAD(P)**+-containing **protein**
AB CsgA is a cell surface protein that plays an essential role in tactile responses during Myxococcus xanthus fruiting body formation by producing the morphogenic C-signal. The primary amino acid sequence of CsgA exhibits homol. with members of the short-chain alc. dehydrogenase (SCAD) family and several lines of evidence suggest that NAD(P)+ **binding** is essential for biol. activity. First, the predicted CsgA secondary **structure** based on the 3.alpha./20.beta.-hydroxysteroid dehydrogenase crystal **structure** suggests that the amino-terminal portion of the **protein** contains an **NAD(P)**+ **binding** pocket. Second, strains with csgA alleles encoding amino acid substitutions T6A and R10A in the NAD(P)+ **binding** pocket failed to develop. Third, exogenous MalE-CsgA rescues csgA development,

whereas MalE-CsgA with the amino acid substitution CsgA T6A does not. Finally, csgA spore yield increased .apprx.20% when buffer contg. 100 nM of MalE-CsgA was supplemented with 10- .mu.M of NAD+ or NADP+. Conversely, 10 .mu.M of NADH or NADPH delayed development for .apprx.24 h and depressed spore levels .apprx.10%. Together, these results argue that NAD(P)+ **binding** is crit. for C-signaling. S135 and K155 are conserved amino acids in the catalytic domain of SCAD members. Strains with csgA alleles encoding the amino acid substitutions S135T or K155R failed to develop. Furthermore, a MalE-CsgA protein contg. CsgA S135T was not able to restore development to csgA cells. In conclusion, amino acids conserved in the coenzyme **binding** pocket and catalytic site are essential for C-signaling.

IT Microorganism development
Myxococcus xanthus
Signal transduction, biological
(a tactile sensory system of Myxococcus xanthus involves an extracellular **NAD(P)**+-contg. **protein**)

IT Proteins, properties
RL: PRP (Properties)
(gene csaA; a tactile sensory system of Myxococcus xanthus involves an extracellular **NAD(P)**+-contg. **protein**)

IT 142298-62-2, Short-chain alcohol dehydrogenase
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(a tactile sensory system of Myxococcus xanthus involves an extracellular **NAD(P)**+-contg. **protein**
homologous with short-chain alc. dehydrogenase)

IT 172726-89-5, Protein (Myxococcus xanthus gene csgA)
RL: PRP (Properties)
(amino acid sequence; a tactile sensory system of Myxococcus xanthus involves an extracellular **NAD(P)**+-contg. **protein**)

L8 ANSWER 18 OF 30 CAPLUS COPYRIGHT 2002 ACS
AN 1995:567243 CAPLUS
DN 123:193725
TI Ascorbate free radical reductase mRNA levels are induced by wounding
AU Grantz, Alexander A.; Brummell, David A.; Bennett, Alan B.
CS Mann Laboratory, Univ. California, Davis, CA, 95616, USA
SO Plant Physiology (1995), 108(1), 411-18
CODEN: PLPHAY; ISSN: 0032-0889
PB American Society of Plant Physiologists
DT Journal
LA English
AB A cDNA clone encoding ascorbate free radical (AFR) reductase (EC 1.6.5.4) was isolated from tomato (Lycopersicon esculentum Mill.) and its mRNA levels were analyzed. The cDNA encoded a deduced protein of 433 amino acids and possessed amino acid domains characteristic of FAD- and **NAD(P)**H-**binding proteins** but did not possess typical eukaryotic targeting sequences, suggesting that it encodes a cytosolic form of AFR reductase. Low-stringency genomic DNA gel blot anal. indicated that a single nuclear gene encoded this enzyme. Total ascorbate contents were greatest in leaves, with decreasing amts. in stems and roots and relatively const. levels in all stages of fruit. AFR reductase activity was inversely correlated with total ascorbate content, whereas the relative abundance of AFR reductase mRNA was directly correlated with enzyme activity in tissues examd. AFR reductase mRNA abundance increased dramatically in response to wounding, a treatment that is known to also induce ascorbate-dependent prolyl hydroxylation required for the accumulation of hydroxyproline-rich glycoproteins. In addn., AFR reductase may contribute to maintaining levels of ascorbic acid for protection against wound-induced free radical-mediated damage. Collectively, the results suggest that AFR reductase activity is regulated at the level of mRNA abundance by low ascorbate contents or by factors that promote ascorbate utilization.

L8 ANSWER 19 OF 30 CAPLUS COPYRIGHT 2002 ACS
AN 1995:430130 CAPLUS
DN 123:50672
TI The use of synthetic peptides for the investigation of components interaction in monooxygenase rabbit liver system
AU Kritsky, A. M.; Kanaeva, I. P.; Davydov, D. R.; Stepanova, N. V.; Bachmanova, G. I.
CS Institute Biomedical Chemistry, Russian Academy Medical Sciences, Moscow, 119832, Russia
SO Cytochrome P450 Int. Conf., 8th (1994), Meeting Date 1993, 477-80. Editor(s): Lechner, Maria Celeste. Publisher: Libbey, Montrouge, Fr. CODEN: 61COAX
DT Conference
LA English
AB Local homol. of NADPH-cytochrome P 450 reductase and cytochrome b5 amino acid sequences allowed the authors to presume structural similarity between the cytochrome c **binding** centers in cytochrome b5 and NADPH-cytochrome P 450 reductase (Davydov, D. R.; et al., 1992). On the basis of this presumption the peptide LEEHPGGEE was synthesized which simulates the part of the cytochrome b5 **binding** center with cytochrome c and cytochrome P 450. The peptide's influence on the NADPH-dependent benzphetamine N-demethylation reaction in a monomeric sol. reconstituted system (MRS), contg. NADPH-cytochrome P 450 reductase, cytochrome P 450 2B4 (2B4) and cytochrome b5, was studied. The action of this **peptide** on **NAD**(**P**)H-cytochrome c reductase activities was studied in microsomes as well. It was shown that it inhibits these reactions, but the process is not highly specific.

L8 ANSWER 20 OF 30 CAPLUS COPYRIGHT 2002 ACS
AN 1994:649166 CAPLUS
DN 121:249166
TI Flavodoxin and NADPH-flavodoxin reductase from Escherichia coli support bovine cytochrome P450c17 hydroxylase activities
AU Jenkins, Christopher M.; Waterman, Michael R.
CS Dep. Biochem., Vanderbilt Univ. Sch. Med., Nashville, TN, 37232-0146, USA
SO Journal of Biological Chemistry (1994), 269(44), 27401-8 CODEN: JBCHA3; ISSN: 0021-9258
DT Journal
LA English
AB Two sol. flavoproteins, purified from Escherichia coli cytosol and identified as flavodoxin and NADPH-flavodoxin (ferredoxin) reductase (flavodoxin reductase) have been found in combination to support the 17.alpha.-hydroxylase activities of heterologously expressed bovine 17.alpha.-hydroxylase cytochrome P 450 (P450c17). Phys. characteristics of the two flavoproteins including absorbance spectra, mol. wts., and amino-terminal sequences are identical with those reported previously for E. coli flavodoxin and flavodoxin reductase. Flavodoxin reductase, possessing FAD as a cofactor, is able to reconstitute P450c17 activities only in the presence of flavodoxin, an FMN-contg. **protein**, and **NAD**(**P**)H. Reducing equiv. are utilized more effectively from NADPH than NADH by flavodoxin reductase. E. coli flavodoxin **binds** P450c17 directly and with relatively high affinity (apparent Ks .apprx. 0.2 .mu.M) at low ionic strength, as evidenced by a change in spin state of the P450c17 heme iron upon titrn. with flavodoxin. This apparent spin shift is attenuated at moderate ionic strengths (100-200mM KCl). In addn., bovine P450c17 **binds** reversibly to flavodoxin Sepharose in an ionic strength-dependent manner. These data implicate charge pairing as being important for the interaction between flavodoxin and P450c17. The authors propose that the amino acid sequence similarity between E. coli flavodoxin-flavodoxin reductase and the putative FMN, FAD, and NAD(P)H **binding** regions of cytochrome P 450 reductase provides the basis for the reconstruction of P450c17 activities by this bacterial system.

L8 ANSWER 21 OF 30 CAPLUS COPYRIGHT 2002 ACS
AN 1994:500887 CAPLUS
DN 121:100887
TI Human NAD(P)H:quinone oxidoreductase2. Gene **structure**, activity, and tissue-specific expression
AU Jaiswal, Anil K.
CS Dep. Pharmacol., Fox Chase Cancer Cent., Philadelphia, PA, 19111, USA
SO Journal of Biological Chemistry (1994), 269(20), 14502-8
CODEN: JBCHA3; ISSN: 0021-9258
DT Journal
LA English
TI Human NAD(P)H:quinone oxidoreductase2. Gene **structure**, activity, and tissue-specific expression
AB Human NAD(P)H:quinone oxidoreductase2 (NQO2) gene, 1336 base pairs (bp) of the 5'-flanking region and 165 bp of the 3'-flanking region, have been sequenced. NQO2 gene is 20 kilobase pairs in length and has seven exons interrupted by six introns as compared to the previously cloned NQO1 gene which contains six exons. The 187 bp of the first exon in the NQO2 gene are noncoding and are absent in the NQO1 gene. The 92 bp of the second exon in the NQO2 gene corresponded to the first exon of the NQO1 gene and so on. The sizes and nucleotide sequences of exons 3-6 are highly conserved between NQO2 and NQO1 genes. The last exon in the NQO2 gene is 1603 bp shorter than the last exon of the NQO1 gene and encodes for 58 amino acids as compared to 101 amino acids encoded by the NQO1 gene. This makes NQO2 protein 43 amino acids shorter than the NQO1 protein. The high degree of conservation between NQO2 and NQO1 gene organization and sequence confirmed that NQO2 gene encodes for a second member of the NQO gene family in human. Nucleotide sequence anal. of the 5'-flanking region of the NQO2 gene revealed presence of four SP1 **binding** sites at positions -214, -170, -106, and -75, a single copy of the antioxidant response element (ARE) at nucleotide -936, and three copies of xenobiotic response element (XRE) at positions -708, -557, and -51. ARE and XRE elements have previously been found in the promoters of the NQO1 and glutathione S-transferase Ya subunit genes and mediate increases in their expression in response to polycyclic arom. compds., phenolic antioxidants, and 2,3,7,8-tetrachlorodibenzyo-p-dioxin (TCDD), resp. The NQO2 cDNA-derived protein in monkey kidney COS1 cells efficiently catalyzed nitroredn. of anti-tumor compd. CB10-200, an analog of nitrophenylaziridine. Northern blot anal. indicates that NQO2 gene is expressed in human heart, brain, lung, liver, and skeletal muscle but does not express in placenta. In contrast, the NQO1 gene was expressed in all human tissues. Large variations were noticed for expression of the NQO2 and NQO1 genes among various tissues. The 1336 bp of the 5'-flanking region of the NQO2 gene contg. ARE and XRE was found sufficient to increase expression of the CAT gene in response to .beta.-naphthoflavone and TCDD in transfected human hepatoblastoma (Hep-G2) cells.
IT **Protein** sequences
(of **NAD(P)**H:quinone oxidoreductase2, of human)

L8 ANSWER 22 OF 30 CAPLUS COPYRIGHT 2002 ACS
AN 1993:468370 CAPLUS
DN 119:68370
TI Light activation and molecular-mass changes of NAD(P)-glyceraldehyde 3-phosphate dehydrogenase of spinach and maize leaves
AU Scagliarini, Sandra; Trost, Paolo; Pupillo, Paolo; Valenti, Vincenzo
CS Dip. Biol., Univ. Bologna, Bologna, I-40126, Italy
SO Planta (1993), 190(3), 313-19
CODEN: PLANAB; ISSN: 0032-0935
DT Journal
LA English
AB Light modulation of chloroplast glyceraldehyde 3-phosphate dehydrogenase (NAD(P)-GAPDH; Ec 1.2.1.13) has been investigated. Complete activation of NADPH-dependent activity was achieved at 25 W.m-2 photosynthetically

active radiation in spinach (Spinacia oleracea) and 100 W.m-2 in maize (Zea mays) leaves. Light activation was stronger in spinach (5-fold on av.) than in maize (2-fold), which shows higher dark activity. The NADH dependent activity did not change appreciably. Several substrate activators can simulate in vitro the light effect with recovery of latent NADPH-dependent activity of spinach enzyme, but they are almost inactive with maize enzyme. A mixt. of activators has been devised to fully activate the spinach enzyme under most conditions. The **NAD(P)**-GAPDH **protein** can be resolved by rapid gel filtration (fast protein liq. chromatog.) into three **conformers** which have different mol. masses according to the light conditions. Enzyme from darkened leaves or chloroplasts, or DCMU-treated chloroplasts is mainly a 600-kDa regulatory form with low NADPH-dependent activity relative to NADH-activity. Enzyme from spinach leaves or chloroplasts during photosynthesis is mainly a 300-kDa oligomer, which along with the 600-kDa form also occurs in leaves of darkened maize. The **conformer** of illuminated maize leaves is mainly a 160-kDa species. Results are consistent with a model of NAD(P)-GAPDH freely interconvertible between protomers of the 160-kDa (or 300-kDa intermediate) form with high NADPH-activity, produced in the light by the action of thioredoxin and activating metabolites (spinach only), and a regulatory 600-kDa **conformer** with lower NADPH-activity produced in darkness or when photosynthesis is inhibited. This behavior is reminiscent of the in-vitro properties of purified enzyme; therefore it seems unlikely that NAD(P)-GAPDH in the chloroplast is part of a stable multienzyme complex or is bound to membranes.

L8 ANSWER 23 OF 30 CAPLUS COPYRIGHT 2002 ACS
AN 1992:230592 CAPLUS
DN 116:230592
TI Characterization of an extremely thermostable glutamate dehydrogenase: a key enzyme in the primary metabolism of the hyperthermophilic archaebacterium, Pyrococcus furiosus
AU Robb, Frank T.; Park, Jae Bum; Adams, Michael W. W.
CS Cent. Mar. Biotechnol., Univ. Maryland, Baltimore, MD, USA
SO Biochimica et Biophysica Acta (1992), 1120(3), 267-72
CODEN: BBACAQ; ISSN: 0006-3002
DT Journal
LA English
IT **Protein** sequences
(of **NAD(P)**-glutamate dehydrogenase N-terminus, of Pyrococcus furiosus)
IT **Conformation** and **Conformers**
(of NAD(P)-glutamate dehydrogenase, of Pyrococcus furiosus, extreme thermal stability of)

L8 ANSWER 24 OF 30 CAPLUS COPYRIGHT 2002 ACS
AN 1992:122291 CAPLUS
DN 116:122291
TI Sequence of a cDNA encoding the bi-specific NAD(P)H-nitrate reductase from the tree Betula pendula and identification of conserved protein regions
AU Friemann, Andreas; Brinkmann, Klaus; Hachtel, Wolfgang
CS Bot. Inst., Univ. Bonn, Bonn, W-5300/1, Germany
SO Molecular and General Genetics (1991), 227(1), 97-105
CODEN: MGGEAE; ISSN: 0026-8925
DT Journal
LA English
AB Nitrate reductase (NR) assays revealed a bi-specific NAD(P)H-NR (EC 1.6.6.2.) to be the only nitrate-reducing enzyme in leaves of hydroponically grown birches. To obtain the primary **structure** of the NAD(P)H-NR, leaf poly (A)+ mRNA was used to construct a cDNA library in the lambda gt11 phage. Recombinant clones were screened with heterologous gene probes encoding NADH-NR from tobacco and squash. A 3.0-kb cDNA was isolated which hybridized to a 3.2-kb mRNA whose level was

significantly higher in plants grown on nitrate than in those grown on ammonia. The nucleotide sequence of the cDNA comprises a reading frame encoding a protein of 898 amino acids which reveals 67%-77% identity with NADH-nitrate reductase sequences from higher plants. To identify conserved and variable regions of the multicenter electron-transfer protein a graphical evaluation of identities found in NR sequence alignments was carried out. Thirteen well-conserved sections exceeding a size of 10 amino acids were found in higher plant nitrate reductases. Sequence comparisons with related redox proteins indicate that about half of the conserved NR regions are involved in cofactor **binding**. The most striking difference in the birch NAD(P)H-NR sequence in comparison to NADH-NR sequences was found at the putative pyridine nucleotide **binding** site. Southern anal. indicates that the bi-specific NR is encoded by a single copy gene in birch.

IT **Protein** sequences
(of **NAD(P)**H nitrate reductase, of Betula pendula, complete)

L8 ANSWER 25 OF 30 CAPLUS COPYRIGHT 2002 ACS
AN 1991:599825 CAPLUS
DN 115:199825
TI Cloning, nucleotide sequence, and transcriptional analysis of the NAD(P)-dependent cholesterol dehydrogenase gene from a Nocardia sp. and its hyperexpression in Streptomyces spp
AU Horinouchi, Sueharu; Ishizuka, Hiroshi; Beppu, Teruhiko
CS Fac. Agric., Univ. Tokyo, Tokyo, 113, Japan
SO Applied and Environmental Microbiology (1991), 57(5), 1386-93
CODEN: AEMIDF; ISSN: 0099-2240
DT Journal
LA English
AB NAD(P)-dependent cholesterol dehydrogenases [NAD(P)-CDH], which allow easier quantification of cholesterol by means of directly measuring the A340 of NAD(P), are useful for clin. purposes. The amino acid sequences of the NH2 terminus and the fragments obtained by CNBr decompn. of the NAD(P)-CDH from a Nocardia sp. were detd. for prepn. of synthetic oligonucleotides as hybridization probes. A 4.4-kbp BamHI fragment hybridizing to these probes was cloned on pUC19 in Escherichia coli. The nucleotide sequence together with the detd. amino acid sequences revealed that this enzyme consists of 364 amino acids (Mr, 39,792) and contains an NAD(P)-**binding** consensus sequence at its NH2-terminal portion. High-resoln. S1 nuclease mapping suggested that in NAD(P)-CDH of both Nocardia and Streptomyces spp. transcription initiates at the adenine residue, which is the first position of the translational initiation triplet (AUG) of this protein. The S1 mapping expts. also showed that cholesterol-dependent regulation in the Nocardia sp. occurred at the level of transcription. In Streptomyces lividans contg. the cloned fragment, however, this promoter was expressed constitutively. DNA manipulation of the cloned gene in E. coli, including the generation of a ribosome-**binding** sequence at an appropriate position by oligonucleotide-directed mutagenesis,led to prodn. of this protein in a very large amt. but in the enzymically inactive form of inclusion bodies. On the other hand, a Streptomyces host-vector system was successfully used for producing 40 times as much enzymically active NAD(P)-CDH as that produced by the original Nocardia sp.

IT **Protein** sequences
(of **NAD(P)**-dependent cholesterol dehydrogenase and precursor, of Nocardia, complete)

L8 ANSWER 26 OF 30 CAPLUS COPYRIGHT 2002 ACS
AN 1990:92923 CAPLUS
DN 112:92923
TI Nucleotide and deduced amino acid sequence of a human cDNA (NQO2) corresponding to a second member of the NAD(P)H:quinone oxidoreductase gene family. Extensive polymorphism at the NQO2 gene locus on chromosome

6
AU Jaiswal, Anil K.; Burnett, Paula; Adesnik, Milton; McBride, O. Wesley
CS Med. Cent., New York Univ., New York, NY, 10016, USA
SO Biochemistry (1990), 29(7), 1899-906
CODEN: BICHAW; ISSN: 0006-2960
DT Journal
LA English
IT **Protein** sequences
(of **NAD**(**P**)H quinone dehydrogenase, of human, complete)
IT 9032-20-6
RL: PRP (Properties)
(isoform to, human gene for, **structure** and mapping and polymorphism of)

L8 ANSWER 27 OF 30 CAPLUS COPYRIGHT 2002 ACS
AN 1988:506976 CAPLUS
DN 109:106976
TI **Structure**-function relationship of NAD(P)H:quinone reductase: characterization of amino-terminal blocking group and essential tyrosine and lysine residues
AU Haniu, Mitsuru; Yuan, Henry; Chen, Shiuan; Iyanagi, Takashi; Lee, Terry D.; Shively, John E.
CS Div. Immunol., Beckman Res. Inst. City of Hope, Duarte, CA, 91010, USA
SO Biochemistry (1988), 27(18), 6877-83
CODEN: BICHAW; ISSN: 0006-2960
DT Journal
LA English
TI **Structure**-function relationship of NAD(P)H:quinone reductase: characterization of amino-terminal blocking group and essential tyrosine and lysine residues
AB The N-terminal-blocked **peptide** of rat liver **NAD**(**P**)H-quinone oxidoreductase [NAD(P)H dehydrogenase (quinone), DT-diaphorase] was detd. by amino acid sequence anal. and by mass spectrometry. The mature protein was composed of 273 amino acids and contained an acetylated N-terminus, which was not identified by previous cDNA anal. The enzyme was inactivated by p-nitrobenzenesulfonyl fluoride (NBSF) or 2,4,6-trinitrobenzenesulfonate (TNBS) with pseudo-1st-order kinetics. These studies suggest that essential tyrosine and lysine may be present in the active site of this enzyme. The NBSF inhibition was protected by 1-naphthol and 1-naphthylamine, but not by NAD. However, TNBS inhibition was not prevented by the naphthalene derivs. or NAD. Specific peptides labeled with NBSF or TNBS were isolated by HPLC and were sequenced. These analyses revealed that the NBSF-labeled tyrosine resides in a predominantly hydrophobic region and TNBS-labeled lysine in a predominantly hydrophlic region.
IT **Protein** sequences
(of **NAD**(**P**)H dehydrogenase (quinone), of rat liver, complete)

L8 ANSWER 28 OF 30 CAPLUS COPYRIGHT 2002 ACS
AN 1988:181215 CAPLUS
DN 108:181215
TI The primary **structure** of the mitochondrial energy-linked nicotinamide nucleotide transhydrogenase deduced from the sequence of cDNA clones
AU Yamaguchi, Mutsuo; Hatefi, Youssef; Trach, Kathleen; Hoch, James A.
CS Dep. Basic Clin. Res., Res. Inst. Scripps Clin., La Jolla, CA, 92037, USA
SO Journal of Biological Chemistry (1988), 263(6), 2761-7
CODEN: JBCHA3; ISSN: 0021-9258
DT Journal
LA English
TI The primary **structure** of the mitochondrial energy-linked nicotinamide nucleotide transhydrogenase deduced from the sequence of cDNA

clones
AB The amino acid sequence of the bovine mitochondrial nicotinamide nucleotide transhydrogenase, which catalyzes hydride ion transfer between NAD(H) and NADP(H) coupled to proton translocation across the mitochondrial inner membrane, was deduced from the corresponding cDNA. Two clones were isolated by screening a bovine phage .lambda.gt10 cDNA library, using 2 synthetic oligonucleotides and a cDNA restriction fragment as probes. The inserts together covered 3105 base pairs of coding sequence, corresponding to 1035 amino acid residues. However, the reading frame at the 5' end was still open. N-terminal sequence anal. of the isolated enzyme indicated the presence of 8 addnl. residues. Thus, the mature transhydrogenase has 1043 amino acid residues and a calcd. mol. wt. of 109,212. The deduced amino acid sequence of the transhydrogenase contained the sequence of 4 tryptic peptides that had been isolated from the enzyme. Two of these were the peptides that had been used for construction of the oligonucleotide probes. The other two were tryptic peptides isolated after labeling the NAD-**binding** site of the transhydrogenase. The central region of the transhydrogenase (residues 420-850) is highly hydrophobic and contains .apprx.14 membrane-spanning segments. By comparison, the N- and the C-terminal regions of the enzyme, which contain the NAD- and the putative NADP-**binding** sites, resp., are relatively hydrophilic and are probably located outside the mitochondrial inner membrane on the matrix side. There is considerable homol. between the bovine enzyme and the Escherichia coli transhydrogenase (2 subunits, .alpha. with Mr = 54,000 and .beta. with Mr = 48,700), whose amino acid sequence has been detd. from the genes.
IT Gene and Genetic element, animal
RL: BIOL (Biological study)
(for nicotinamide nucleotide transhydrogenase, of cattle mitochondria, **structure** of)
IT Mitochondria
(nicotinamide and nucleotide transhydrogenase of, of cattle, **structure** of cDNA for)
IT Cattle
(nicotinamine nucleotide transhydrogenase of mitochondria of, **structure** of cDNA for)
IT **Protein** sequences
(of **NAD(P)** transhydrogenase, of cattle mitochondria, complete)
IT 9014-18-0, Nicotinamide nucleotide transhydrogenase
RL: PRP (Properties)
(of mitochondria of cattle, **structure** of cDNA for)

L8 ANSWER 29 OF 30 CAPLUS COPYRIGHT 2002 ACS
AN 1987:454250 CAPLUS
DN 107:54250
TI Anion transport in rat brain mitochondria: fumarate uptake via the dicarboxylate carrier
AU Passarella, Salvatore; Atlante, Anna; Barile, Maria; Quagliariello, Ernesto
CS Cent. Stud. Mitocondri Metab., Univ. Bari, Bari, 70126, Italy
SO Neurochemical Research (1987), 12(3), 255-64
CODEN: NEREDZ; ISSN: 0364-3190
DT Journal
LA English
AB The penetration of fumarate into rat brain mitochondria was investigated, as required in brain ammoniogenesis. Mitochondria swelled in ammonium fumarate, and this swelling was increased by both phosphate (Pi) and malate. According to a carrier-mediated process, fumarate translocation, which occurs in exchange with intramitochondrial malate or Pi shows satn. characteristics. By photometrically investigating the kinetics of fumarate/malate, fumarate/Pi, and malate/Pi exchanges, different Km values were obtained (10, 22, and 250 .mu.M, resp.), whereas no significant difference was found for Vmax values (40 nmol **NAD(P)**

reduced/min/mg **protein**). This suggested that fumarate and malate share a single carrier to enter mitochondria, namely the dicarboxylate carrier. Both comparison made of the Vmax values and inhibition studies excluded a fumarate translocation via either the tricarboxylate carrier, whose occurrence in brain is here demonstrated, or oxodicarboxylate carrier. Kinetic investigation of the dicarboxylate translocator showed the existence of SH group(s) and metal ion(s) at or near the substrate-**binding** sites. The exptl. findings are discussed in the light of fumarate uptake in vivo in brain ammoniogenesis.

L8 ANSWER 30 OF 30 CAPLUS COPYRIGHT 2002 ACS
AN 1974:45176 CAPLUS
DN 80:45176
TI Glutamate dehydrogenase. Modification of the distribution of polyhexamers by coenzymes and specific effectors
AU Dessen, Philippe; Pantaloni, Dominique
CS Lab. Enzymol., CNRS, Gif-sur-Yvette, Fr.
SO European Journal of Biochemistry (1973), 39(1), 157-69
CODEN: EJBCAI; ISSN: 0014-2956
DT Journal
LA French
AB The effects of the coenzymes NAD(P) and NAD(P)H and the effectors ADP and GTP on the polyhexameric **structure** of pig liver glutamate dehydrogenase (EC 1.4.1.3) (I) was investigated. The increase in the dp of I with the **binding** of NAD(P)H was explained by a higher affinity of the coenzymes for the protomers which have an assocd. area compared to the protomers which have a free area. No variation was obsd. with NAD(P), ADP, or GTP alone. The formation of the **protein** .cntdot.GTP.cntdot.**NAD**(**P**)H ternary complex led to a complete depolymn. when the two ligands were in satg. concns. The systematic study of the variations of polymn. in terms of increasing concn. of NAD(P)H at const. concn. of GTP, or in terms of increasing concn. of GTP at const. concn. of NAD(P)H showed that the interaction between the two opposite protomers of two consecutive hexamers were responsible for the sigmoidal shape of the depolymn. curves. The reversibility of this effect by ADP was assigned to a competition between the **binding** of ADP and GTP.
IT 53-57-6 53-59-8 53-84-9 58-64-0, biological studies 58-68-4 86-01-1
RL: BIOL (Biological study)
(glutamate dehydrogenase polyhexameric **structure** in presence of)
IT 9029-12-3
RL: PRP (Properties)
(polyhexameric **structure** of, coenzymes and effectors in)

AN 1996:573121 CAPLUS
DN **125:240912**
TI The nicotinamide dinucleotide binding motif: a comparison of nucleotide binding proteins
AU Bellamacina, Cornelia R.
CS Rosenstiel Basic Medical Sciences Research Center, Brandeis University, Waltham, MA, 02254-9110, USA
SO FASEB Journal (1996), 10(11), 1257-1269
CODEN: FAJOEC; ISSN: 0892-6638
PB Federation of American Societies for Experimental Biology
DT Journal; General Review
LA English
AB A review with 47 refs. Classical NAD (NAD+) binding proteins contain a .beta..alpha..beta..alpha..beta. unit. By comparing 14 such proteins, it is obsd. that an addnl. .beta. strand assocs. with this unit to form the core topol., the min. structure necessary to bind cofactor. Although the overall topologies of the cofactor binding domains of nicotinamide binding proteins vary, they all contain at least the core topol. The first 30-35 amino acids of the core topol., called the fingerprint region, are diagnostic for the presence of a dinucleotide binding fold. There are four characteristics of this fingerprint region: (1) a phosphate binding consensus sequence, GXGXXG, (2) six positions usually occupied by small hydrophobic amino acids, (3) a conserved, neg. charged residue (Glu or Asp) at the end of the second .beta. strand of the fingerprint region, and (4) a conserved pos. charged residue (Arg or Lys) at the beginning of the first .beta. strand of the fingerprint region. The core topologies of the classical nicotinamide binding proteins overlap well with root mean squared deviations of main chain atoms ranging from 0.7 to 4.7 .ANG.. A conserved interaction (found in 8 of the 12 classical nicotinamide binding proteins studied) between the cofactor and the protein is a hydrogen bond between the pyrophosphate oxygen of NAD(P)+ and the carboxy-terminal glycine of the phosphate binding helix, the first .alpha. helix of the .beta..alpha..beta..alpha..beta. unit. The classical nicotinamide binding proteins all bind their cofactor in the same location and orientation, with the cofactor itself adopting a similar extended conformation in every structure. Although obsd. less frequently than the classical fold, numerous nonclassical folding patterns are also used by proteins that bind NAD(P)+.